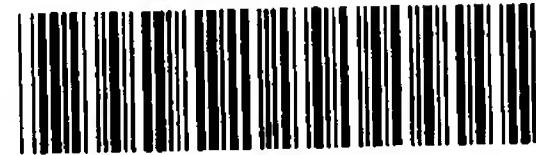


C. 105



OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/038,224

DATE: 01/28/2002
TIME: 17:55:27

Input Set : A:\00033316.txt
Output Set: N:\CRF3\01282002\J038224.raw

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3 <110> APPLICANT: Schewe et al
 5 <120> TITLE OF INVENTION: Monocotyledon plant cells and plants which synthesise
 modified starch
 7 <130> FILE REFERENCE: 514413-3900
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/038,224
 C--> 10 <141> CURRENT FILING DATE: 2001-10-19
 12 <150> PRIOR APPLICATION NUMBER: DE 10052492.3
 13 <151> PRIOR FILING DATE: 2000-10-23
 15 <150> PRIOR APPLICATION NUMBER: DE 10064805.3
 16 <151> PRIOR FILING DATE: 2000-12-22
 18 <160> NUMBER OF SEQ ID NOS: 16
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 5061
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Solanum tuberosum
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (216)..(4607)
 31 <400> SEQUENCE: 1
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 36 cgaatttctc gagcgttctt cgctaatttc ctcgttactt cactagaaaat cgacgtttct 180
 38 agctgaacctt gaggtaattt agccagtggg aggtatg agt aat tcc tta ggg 233
 Met Ser Asn Ser Leu Gly
 39 1 5
 40 10 281
 42 aat aac ttg ctg tac cag gga ttc cta acc tca aca gtg ttg gaa cat 281
 43 Asn Asn Leu Leu Tyr Gln Gly Phe Leu Thr Ser Thr Val Leu Glu His
 44 15 20
 46 aaa agt aga atc agt cct tgt gtt gga ggc aat tct ttg ttt caa 329
 47 Lys Ser Arg Ile Ser Pro Pro Cys Val Gly Gly Asn Ser Leu Phe Gln
 48 25 30 35
 50 caa caa gtg atc tcg aaa tca cct tta tca act gag ttt cga ggt aac 377
 51 Gln Gln Val Ile Ser Lys Ser Pro Leu Ser Thr Glu Phe Arg Gly Asn
 52 40 45 50
 54 agg tta aag gtg cag aaa aag aaa ata cct atg gga aag aac cgt gct 425
 55 Arg Leu Lys Val Gln Lys Lys Ile Pro Met Gly Lys Asn Arg Ala
 56 55 60 65 70
 59 ttt tct agt tct cct cat gct gta ctt acc act gat acc tct tct gag 473
 60 Phe Ser Ser Ser Pro His Ala Val Leu Thr Thr Asp Thr Ser Ser Glu
 61 75 80 85
 63 cta gca gaa aag ttc agt cta gaa ggg aat att gag cta cag gtt gat 521
 64 Leu Ala Glu Lys Phe Ser Leu Glu Gly Asn Ile Glu Leu Gln Val Asp
 65 90 95 100

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68	Val	Arg	Pro	Pro	Thr	Ser	Gly	Asp	Val	Ser	Phe	Val	Asp	Phe	Gln	Ala				
69	105								110						115					
71	aca	aat	ggt	agt	gat	aaa	ctg	ttt	ttg	cac	tgg	ggg	gca	gta	aag	ttc	617			
72	Thr	Asn	Gly	Ser	Asp	Lys	Leu	Phe	Leu	His	Trp	Gly	Ala	Val	Lys	Phe				
73	120								125						130					
75	gga	aaa	gaa	aca	tgg	tct	ctt	cct	aat	gat	cgt	cca	gat	ggg	acc	aaa	665			
76	Gly	Lys	Glu	Thr	Trp	Ser	Leu	Pro	Asn	Asp	Arg	Pro	Asp	Gly	Thr	Lys				
77	135								140				145		150					
79	gtg	tac	aag	aac	aaa	gca	ctt	aga	act	cca	ttt	gtt	aaa	tct	ggc	tct	713			
80	Val	Tyr	Lys	Asn	Lys	Ala	Leu	Arg	Thr	Pro	Phe	Val	Lys	Ser	Gly	Ser				
81	155								160						165					
83	aac	tcc	atc	ctg	aga	ctg	gag	ata	cg	gac	act	gct	atc	gaa	gct	att	761			
84	Asn	Ser	Ile	Leu	Arg	Leu	Glu	Ile	Arg	Asp	Thr	Ala	Ile	Glu	Ala	Ile				
85	170								175						180					
87	gag	ttt	ctc	ata	tac	gat	gaa	gcc	tac	gat	aaa	tgg	ata	aag	aat	aat	809			
88	Glu	Phe	Leu	Ile	Tyr	Asp	Glu	Ala	Tyr	Asp	Lys	Trp	Ile	Lys	Asn	Asn				
89	185								190						195					
91	gg	t	gc	a	at	tt	cg	t	gc	aaa	ttg	tca	aga	aaa	gag	ata	cga	ggc	cca	857
92	Gly	Gly	Asn	Phe	Arg	Val	Lys	Leu	Ser	Arg	Lys	Glu	Ile	Arg	Gly	Pro				
93	200								205						210					
95	gat	gtt	tca	gtt	cct	gag	gag	ctt	gta	cag	atc	caa	tca	tat	ttg	agg	905			
96	Asp	Val	Ser	Val	Pro	Glu	Glu	Leu	Val	Gln	Ile	Gln	Ser	Tyr	Leu	Arg				
97	215								220				225		230					
99	tgg	gag	agg	aag	gga	aaa	cag	aat	tac	acc	cct	gag	aaa	gag	aag	gag	953			
100	Trp	Glu	Arg	Lys	Gly	Lys	Gln	Asn	Tyr	Thr	Pro	Glu	Lys	Glu	Lys	Glu				
101	235								240						245					
103	gaa	tat	gag	gct	gct	cga	act	gag	cta	cag	gag	gaa	ata	gct	cgt	gg	1001			
104	Glu	Tyr	Glu	Ala	Ala	Arg	Thr	Glu	Leu	Gln	Glu	Glu	Ile	Ala	Arg	Gly				
105	250								255						260					
107	gct	tcc	ata	cag	gac	att	cga	gca	agg	cta	aca	aaa	act	aat	gat	aaa	1049			
108	Ala	Ser	Ile	Gln	Asp	Ile	Arg	Ala	Arg	Leu	Thr	Lys	Thr	Asn	Asp	Lys				
109	265								270						275					
111	agt	caa	agc	aaa	gaa	gag	cct	ctt	cat	gta	aca	aag	agt	gaa	ata	cct	1097			
112	Ser	Gln	Ser	Lys	Glu	Glu	Pro	Leu	His	Val	Thr	Lys	Ser	Glu	Ile	Pro				
113	280								285						290					
115	gat	gac	ctt	gcc	caa	gca	caa	gct	tac	att	agg	tgg	gag	aaa	gca	gga	1145			
116	Asp	Asp	Leu	Ala	Gln	Ala	Gln	Ala	Tyr	Ile	Arg	Trp	Glu	Lys	Ala	Gly				
117	295								300				305		310					
120	aag	ccg	aac	tat	cct	cca	gaa	aag	caa	att	gaa	gaa	ctc	gaa	gaa	gca	1193			
121	Lys	Pro	Asn	Tyr	Pro	Pro	Glu	Lys	Gln	Ile	Glu	Glu	Leu	Glu	Glu	Ala				
122	315								320						325					
124	aga	aga	gaa	ttg	caa	ctt	gag	ctt	gag	aaa	ggc	att	acc	ctt	gat	gag	1241			
125	Arg	Arg	Glu	Leu	Gln	Leu	Glu	Leu	Glu	Lys	Gly	Ile	Thr	Leu	Asp	Glu				
126	330								335						340					
128	ttg	cg	aaa	aag	att	aca	aaa	gg	gag	ata	aaa	act	aag	g	cg	gaa	aag	1289		
129	Leu	Arg	Lys	Lys	Ile	Thr	Lys	Gly	Glu	Ile	Lys	Thr	Lys	Ala	Glu	Lys				
130	345								350						355					
132	cac	gtg	aaa	aga	agc	tct	ttt	gcc	gtt	gaa	aga	atc	caa	aga	aag	aag	1337			

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136	aga gac ttt ggg cag ctt att aat aag tat cct tcc agt cct gca gta	1385		
137	Arg Asp Phe Gly Gln Leu Ile Asn Lys Tyr Pro Ser Ser Pro Ala Val			
138	375	380	385	390
140	caa gta caa aag gtc ttg gaa gaa cca cca gcc tta tct aaa att aag	1433		
141	Gln Val Gln Lys Val Leu Glu Glu Pro Pro Ala Leu Ser Lys Ile Lys			
142	395	400	405	
144	ctg tat gcc aag gag aag gag gag cag att gat gat ccg atc ctt aat	1481		
145	Leu Tyr Ala Lys Glu Lys Glu Glu Gln Ile Asp Asp Pro Ile Leu Asn			
146	410	415	420	
148	aaa aag atc ttt aag gtc gat gat ggg gag cta ctg gta ctg gta gca	1529		
149	Lys Lys Ile Phe Lys Val Asp Asp Gly Glu Leu Leu Val Leu Val Ala			
150	425	430	435	
152	aag tcc tct ggg aag aca aaa gta cat ata gct aca gat ctg aat cag	1577		
153	Lys Ser Ser Gly Lys Thr Lys Val His Ile Ala Thr Asp Leu Asn Gln			
154	440	445	450	
156	cca att act ctt cac tgg gca tta tcc aaa agt cgt gga gag tgg atg	1625		
157	Pro Ile Thr Leu His Trp Ala Leu Ser Lys Ser Arg Gly Glu Trp Met			
158	455	460	465	470
160	gta cca cct tca agc ata ttg cct cct gga tca att att tta gac aag	1673		
161	Val Pro Pro Ser Ser Ile Leu Pro Pro Gly Ser Ile Ile Leu Asp Lys			
162	475	480	485	
164	gct gcc gaa aca cct ttt tcc gcc agt tct tct gat ggt cta act tct	1721		
165	Ala Ala Glu Thr Pro Phe Ser Ala Ser Ser Ser Asp Gly Leu Thr Ser			
166	490	495	500	
168	aag gta caa tct ttg gat ata gta att gaa gat ggc aat ttt gtg ggg	1769		
169	Lys Val Gln Ser Leu Asp Ile Val Ile Glu Asp Gly Asn Phe Val Gly			
170	505	510	515	
172	atg cca ttt gtt ctt ttg tct ggt gaa aaa tgg att aag aac caa ggg	1817		
173	Met Pro Phe Val Leu Leu Ser Gly Glu Lys Trp Ile Lys Asn Gln Gly			
174	520	525	530	
176	tcg gat ttc tat gtt gac ttc agt gct gca tcc aaa tta gca ctc aag	1865		
177	Ser Asp Phe Tyr Val Asp Phe Ser Ala Ala Ser Lys Leu Ala Leu Lys			
178	535	540	545	550
181	gct gct ggg gat ggc agt gga act gca aag tct tta ctg gat aaa ata	1913		
182	Ala Ala Gly Asp Gly Ser Gly Thr Ala Lys Ser Leu Leu Asp Lys Ile			
183	555	560	565	
185	gca gat atg gaa agt gag gct cag aag tca ttt atg cac cgg ttt aat	1961		
186	Ala Asp Met Glu Ser Glu Ala Gln Lys Ser Phe Met His Arg Phe Asn			
187	570	575	580	
189	att gct gct gac ttg ata gaa gat gcc act agt gct ggt gaa ctt ggt	2009		
190	Ile Ala Ala Asp Leu Ile Glu Asp Ala Thr Ser Ala Gly Glu Leu Gly			
191	585	590	595	
193	ttt act gga att ctt gta tgg atg agg ttc atg gct aca agg caa ctg	2057		
194	Phe Thr Gly Ile Leu Val Trp Met Arg Phe Met Ala Thr Arg Gln Leu			
195	600	605	610	
197	ata tgg aac aaa aac tat aac gta aaa cca cgt gaa ata agc aag gct	2105		
198	Ile Trp Asn Lys Asn Tyr Asn Val Lys Pro Arg Glu Ile Ser Lys Ala			

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202	Gln Asp Arg Leu Thr Asp Leu Leu Gln Asn Ala Phe Thr Ser His Pro				
203	635	640	645		
205	caa tac cgt gaa att ttg cgg atg att atg tca act gtt gga cgt gga				2201
206	Gln Tyr Arg Glu Ile Leu Arg Met Ile Met Ser Thr Val Gly Arg Gly				
207	650	655	660		
209	ggt gaa ggg gat gta gga cag cga att agg gat gaa att ttg gtc atc				2249
210	Gly Glu Gly Asp Val Gly Gln Arg Ile Arg Asp Glu Ile Leu Val Ile				
211	665	670	675		
213	cag agg aaa aat gac tgc aag ggt ggt atg atg gaa gaa tgg cat cag				2297
214	Gln Arg Lys Asn Asp Cys Lys Gly Gly Met Met Glu Glu Trp His Gln				
215	680	685	690		
217	aaa ttg cat aat aat act agt cct gat gat gtt gtg atc tgt cag gca				2345
218	Lys Leu His Asn Asn Thr Ser Pro Asp Asp Val Val Ile Cys Gln Ala				
219	695	700	705	710	
221	ttg att gac tac atc aag agt gat ttt gat ctt ggt gtt tat tgg aaa				2393
222	Leu Ile Asp Tyr Ile Lys Ser Asp Phe Asp Leu Gly Val Tyr Trp Lys				
223	715	720	725		
225	acc ctg aat gag aac gga ata aca aaa gag cgt ctt ttg agt tat gac				2441
226	Thr Leu Asn Glu Asn Gly Ile Thr Lys Glu Arg Leu Leu Ser Tyr Asp				
227	730	735	740		
229	cgt gct atc cat tct gaa ccg aat ttt aga gga gat caa aag aat ggt				2489
230	Arg Ala Ile His Ser Glu Pro Asn Phe Arg Gly Asp Gln Lys Asn Gly				
231	745	750	755		
233	ctt ttg cgt gat tta ggt cac tat atg aga aca ttg aag gct gtt cat				2537
234	Leu Leu Arg Asp Leu Gly His Tyr Met Arg Thr Leu Lys Ala Val His				
235	760	765	770		
237	tca ggt gca gat ctt gag tct gct att gca aac tgc atg ggc tac aaa				2585
238	Ser Gly Ala Asp Leu Glu Ser Ala Ile Ala Asn Cys Met Gly Tyr Lys				
239	775	780	785	790	
242	act gag gga gaa ggc ttt atg gtt gga gtc cag ata aat cct gta tca				2633
243	Thr Glu Gly Glu Gly Phe Met Val Gly Val Gln Ile Asn Pro Val Ser				
244	795	800	805		
246	ggc ttg cca tct ggc ttt cag ggc ctc ctc cat ttt gtc tta gac cat				2681
247	Gly Leu Pro Ser Gly Phe Gln Gly Leu Leu His Phe Val Leu Asp His				
248	810	815	820		
250	gtg gaa gat aaa aat gtg gaa act ctt ctt gag gga ttg cta gag gct				2729
251	Val Glu Asp Lys Asn Val Glu Thr Leu Leu Glu Gly Leu Leu Glu Ala				
252	825	830	835		
254	cgt gag gag ctt agg ccc ttg ctt ctc aaa cca aac aac cgt cta aag				2777
255	Arg Glu Glu Leu Arg Pro Leu Leu Lys Pro Asn Asn Arg Leu Lys				
256	840	845	850		
258	gat ctg ctg ttt ttg gac ata gca ctt gat tct aca gtt aga aca gca				2825
259	Asp Leu Leu Phe Leu Asp Ile Ala Leu Asp Ser Thr Val Arg Thr Ala				
260	855	860	865	870	
262	gta gaa agg gga tat gaa gaa ttg aac aac gct aat cct gag aaa atc				2873
263	Val Glu Arg Gly Tyr Glu Glu Leu Asn Asn Ala Asn Pro Glu Lys Ile				
264	875	880	885		

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266 atg tac ttc atc tcc ctc gtt ctt gaa aat ctc gca ctc tct gtg gac	2921
267 Met Tyr Phe Ile Ser Leu Val Leu Glu Asn Leu Ala Leu Ser Val Asp	
268 890 895 900	
270 gat aat gaa gat ctt gtt tat tgc ttg aag gga tgg aat caa gct ctt	2969
271 Asp Asn Glu Asp Leu Val Tyr Cys Leu Lys Gly Trp Asn Gln Ala Leu	
272 905 910 915	
274 tca atg tcc aat ggt gga gac aac cat tgg gct tta ttt gca aaa gct	3017
275 Ser Met Ser Asn Gly Gly Asp Asn His Trp Ala Leu Phe Ala Lys Ala	
276 920 925 930	
278 gta ctt gac aga atc cgt ctt gca ctt gca agc aag gca gag tgg tac	3065
279 Val Leu Asp Arg Ile Arg Leu Ala Leu Ala Ser Lys Ala Glu Trp Tyr	
280 935 940 945 950	
282 cat cac tta ttg cag cca tct gcc gaa tat cta gga tca atc ctt ggg	3113
283 His His Leu Leu Gln Pro Ser Ala Glu Tyr Leu Gly Ser Ile Leu Gly	
284 955 960 965	
286 gtg gac caa tgg gct ttg aac ata ttt act gaa gaa att ata cgt gct	3161
287 Val Asp Gln Trp Ala Leu Asn Ile Phe Thr Glu Glu Ile Ile Arg Ala	
288 970 975 980	
290 gga tca gca gct tca tta tcc tct ctt ctt aat aga ctc gat ccc gtg	3209
291 Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu Asn Arg Leu Asp Pro Val	
292 985 990 995	
294 ctt cgg aaa act gca aat cta gga agt tgg cag att atc agt cca gtt	3257
295 Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp Gln Ile Ile Ser Pro Val	
296 1000 1005 1010	
298 gaa gcc gtt gga tat gtt gtc gtt gtg gat gag ttg ctt tca gtt cag	3305
299 Glu Ala Val Gly Tyr Val Val Val Val Asp Glu Leu Leu Ser Val Gln	
300 1015 1020 1025 1030	
303 aat gaa atc tac aag aag ccc acg atc tta gta gca aac tct gtt aaa	3353
304 Asn Glu Ile Tyr Lys Lys Pro Thr Ile Leu Val Ala Asn Ser Val Lys	
305 1035 1040 1045	
307 gga gag gag gaa att cct gat ggt gct gtt gcc ctg ata aca cca gac	3401
308 Gly Glu Glu Glu Ile Pro Asp Gly Ala Val Ala Leu Ile Thr Pro Asp	
309 1050 1055 1060	
311 atg cca gat gtt ctt tca cat gtt tct gtt cga gct aga aat ggg aag	3449
312 Met Pro Asp Val Leu Ser His Val Ser Val Arg Ala Arg Asn Gly Lys	
313 1065 1070 1075	
315 gtt tgc ttt gct aca tgc ttt gat ccc aat ata ttg gct gac ctc caa	3497
316 Val Cys Phe Ala Thr Cys Phe Asp Pro Asn Ile Leu Ala Asp Leu Gln	
317 1080 1085 1090	
319 gca aag gaa gga agg att ttg ctc tta aag cct aca cct tca gac ata	3545
320 Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys Pro Thr Pro Ser Asp Ile	
321 1095 1100 1105 1110	
323 atc tat agt gag gtg aat gag att gag ctc caa agt tca agt aac ttg	3593
324 Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu Gln Ser Ser Asn Leu	
325 1115 1120 1125	
327 gta gaa gct gaa act tca gca aca ctt aga ttg gtg aaa aag caa ttt	3641
328 Val Glu Ala Glu Thr Ser Ala Thr Leu Arg Leu Val Lys Lys Gln Phe	
329 1130 1135 1140	
331 ggt ggt tgt tac gca ata tca gca gat gaa ttc aca agt gaa atg gtt	3689

VERIFICATION SUMMARY
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L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date